

SEQUENCE LISTING

<110> GARABEDIAN, Michael
TANEJA, Samir
HITTELMAN, Adam
MARKUS, Steven

<120> METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES

<130> GARABEDIAN=1.1A

<140> NOT YET ASSIGNED

<141> 2001-03-26

<150> 60/225,618

<151> 2000-08-15

<150> 60/191,768

<151> 2000-03-24

<160> 20

<170> PatentIn version 3.0

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<211> 474

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<212> PRT

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<400> 2

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20 25 30

Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys

35	40	45
Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His		
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Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp		
65	70	75
Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly		
85	90	95
Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg		
100	105	110
Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser		
115	120	125
Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu		
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Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His		
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 <212> PRT
 <213> Human

<400> 4

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Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
 20 25 30

Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
 35 40 45

Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
 50 55 60

Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
 65 70 75 80

Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
 85 90 95

Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys
 100 105 110

Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
 115 120 125

Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
 130 135 140

Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
 145 150 155 160

Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
 165 170 175

Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
 180 185 190

Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
 195 200 205

Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
 210 215 220

Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
 225 230 235 240

Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
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Asp Ser Glu Gly Ser Val Tyr Phe
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<220>
 <221> misc_feature
 <223> n at position 65 is unknown.

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 gggcgcgmgaa aaagggggccc ggccggagacc aagggcagcg gcggcccgca agggcgccgg 240
 ggaagcgccc cggaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac 300
 acacgagcgc gagccgccac aacaccacac ccggcccaag gagaacagca cgccaacgcg 360
 ccagycacgg cgggcacggg aggcggggcca cacacagcgg ccccgccaag gcacggcgca 420
 cggcacaagg gcaccacgcg agacaagcga ggaggcagca cgccgagacc ggccggaggg 480
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 <212> PRT
 <213> Human

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 35 40 45
 Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
 50 55 60
 Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
 65 70 75 80
 Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
 85 90 95
 Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
 100 105 110
 Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
 115 120 125
 Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
 130 135 140

Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
145 150 155 160

Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
165 170 175

Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
180 185

<210> 7

<211> 126

<212> DNA

<213> Human

<400> 7

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ccctcgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt 120

caagga 126

<210> 8

<211> 42

<212> PRT

<213> Human

<400> 8

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Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
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Ala Pro Cys His Arg Lys Gly Leu Gln Gly
35 40

<210> 9

<211> 678

<212> DNA

<213> Human

<220>

<221> misc_feature

<223> n at position 651 is unknown.

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caccacccaa caatgactaa tcaaaactaac ctcaaaacaa atgataacca tacacaacac 180

taaaggacga acctgatctc ttatactagt atccttaate atttttattg ccacaactaa 240

ctcctcggga ctccctgcctc actcatttac accaaccacc caactatcta taaacctago 300

catggccatc cccttatgag cgggcgcagt gattatagcg ttctgcctca agattaaaaa 360

tgccctagcc cacttcttac cacaaggcac acctacaccc cttatcccca tactagttat 420

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cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tatcctagaa 600
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<213> Human
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<400> 10
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20 25 30
Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln
35 40 45
Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His
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<210> 11
<211> 1918
<212> DNA
<213> Human
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agcctaactt ttcatacaggc aatacatact ggagagaaac cttacaaatg tcatgaatgc 180
ggcaagggtt ttaggcaciaa ttcatacctt gcaactcatc ggcaaatca tactggagag 240
aaaccttaca agtgtaatga gtgtgggaaa gccttttagt tgcatcctaa cctaactacc 300
cataagggtc tccatactgg agagaagcct tacaaatgta atcaatgttg caaggtcttc 360
actcagaact cacaccttgc aaatcatcaa aggactcaca ccggagagaa accttaccca 420
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cacctggcaa atcaccgaag aattcatact ggggagaaac cttacagggtg tacagagtgt 600
gggaaagcct ttagggttaag atcaagtcta actaccata tggcaatcca cactggagaa 660
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catcacagaa tgcataccgg agagaaacct tacaaatgag tgtggtgagg tcattaggtg 780
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<210> 12
<211> 252
<212> PRT
<213> Human

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<400> 12
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          20          25          30

Gly Arg Ala Phe Ser Asp Arg Ser Ser Leu Thr Phe His Gln Ala Ile
          35          40          45

His Thr Gly Glu Lys Pro Tyr Lys Cys His Glu Cys Gly Lys Val Phe
50          55          60

Arg His Asn Ser Tyr Leu Ala Thr His Arg Arg Ile His Thr Gly Glu
65          70          75          80

Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Met His Ser
          85          90          95

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Asn Leu Thr Thr His Lys Val Ile His Thr Gly Glu Lys Pro Tyr Lys
100 105 110

Cys Asn Gln Cys Gly Lys Val Phe Thr Gln Asn Ser His Leu Ala Asn
115 120 125

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Asn Glu Cys
130 135 140

Gly Lys Ala Phe Ser Val Arg Ser Ser Leu Thr Thr His Gln Ala Ile
145 150 155 160

His Thr Gly Lys Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe
165 170 175

Thr Gln Asn Ala His Leu Ala Asn His Arg Arg Ile His Thr Gly Glu
180 185 190

Lys Pro Tyr Arg Cys Thr Glu Cys Gly Lys Ala Phe Arg Val Arg Ser
195 200 205

Ser Leu Thr Thr His Met Ala Ile His Thr Gly Glu Lys Arg Tyr Lys
210 215 220

Cys Asn Glu Cys Gly Lys Val Phe Arg Gln Ser Ser Asn Leu Ala Ser
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His His Arg Met His Thr Gly Glu Lys Pro Tyr Lys
245 250

<210> 13

<211> 8588

<212> DNA

<213> Human

<400> 13

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Cys Ala Val Cys Asn Lys Phe Thr Thr Asp Asn Leu Asp Met Leu Gly
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Leu His Met Asn Val Glu Arg Ser Leu Ser Glu Asp Glu Trp Lys Ala
50     55     60
Val Met Gly Asp Ser Tyr Gln Cys Lys Leu Cys Arg Tyr Asn Thr Gln
65     70     75     80
Leu Lys Ala Asn Phe Gln Leu His Cys Lys Thr Asp Lys His Val Gln
85     90     95
Lys Tyr Gln Leu Val Ala His Ile Lys Glu Gly Gly Lys Ala Asn Glu
100    105    110
Trp Arg Leu Lys Cys Val Ala Ile Gly Asn Pro Val His Leu Lys Cys
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Asn Ala Cys Asp Tyr Tyr Thr Asn Ser Leu Glu Lys Leu Arg Leu His
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Thr Val Asn Ser Arg His Glu Ala Ser Leu Lys Leu Tyr Lys His Leu
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Gln Gln His Glu Ser Gly Val Glu Gly Glu Ser Cys Tyr Tyr His Cys
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Val Leu Cys Asn Tyr Ser Thr Lys Ala Lys Leu Asn Leu Ile Gln His
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Val Arg Ser Met Lys His Gln Arg Ser Glu Ser Leu Arg Lys Leu Gln
195    200    205
Arg Leu Gln Lys Gly Leu Pro Glu Glu Asp Glu Asp Leu Gly Gln Ile
210    215    220
Phe Thr Ile Arg Arg Cys Pro Ser Thr Asp Pro Glu Glu Ala Ile Glu
225    230    235    240

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 Lys Asp Gln Glu Gly Gly Ala Ser Ser Ser Gln Ala Glu Lys Glu Leu
 260 265 270
 Thr Asp Ser Pro Ala Thr Ser Lys Arg Ile Ser Phe Pro Gly Ser Ser
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 Glu Ser Pro Leu Ser Ser Lys Arg Pro Lys Thr Ala Glu Glu Ile Lys
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 Pro Glu Gln Met Tyr Gln Cys Pro Tyr Cys Lys Tyr Ser Asn Ala Asp
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Leu Lys Ser His Gln Glu His Val His Gln Asn Tyr Phe Pro Phe
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Lys Gln Leu Glu Arg Phe Ala Lys Gln Tyr Arg Asp His Tyr Asp
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